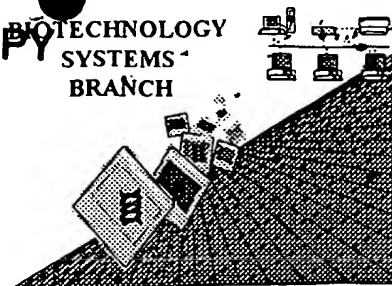


BEST AVAILABLE COPY

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/930,440
Source: OIPE
Date Processed by STIC: 08/23/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/930,440

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 ✓ Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/930,440

DATE: 08/23/2001

TIME: 16:49:26

Input Set : A:\PF509p2--SeqList.txt

Output Set: N:\CRF3\08162001\I930440.raw

2 <110> APPLICANT: Betenbaugh et al.
 4 <120> TITLE OF INVENTION: Engineering Intracellular Sialylation Pathways
 6 <130> FILE REFERENCE: PF509P2
 C--> 8 <140> CURRENT APPLICATION NUMBER: US/09/930,440
 C--> 9 <141> CURRENT FILING DATE: 2001-08-16
 11 <150> PRIOR APPLICATION NUMBER: 60/227,579
 12 <151> PRIOR FILING DATE: 2000-08-25
 14 <150> PRIOR APPLICATION NUMBER: 09/516,793
 15 <151> PRIOR FILING DATE: 2000-03-01
 17 <150> PRIOR APPLICATION NUMBER: 60/169,624
 18 <151> PRIOR FILING DATE: 1999-12-08
 20 <150> PRIOR APPLICATION NUMBER: 60/122,582
 21 <151> PRIOR FILING DATE: 1999-03-02
 23 <160> NUMBER OF SEQ ID NOS: 8
 25 <170> SOFTWARE: PatentIn Ver. 2.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 1429
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo sapiens
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (1)..(693)
 36 <400> SEQUENCE: 1
 37 atg gcc ttc cca aag aag aaa ctt cag ggt ctt gtg gct gca acc atc 48
 38 Met Ala Phe Pro Lys Lys Lys Leu Gln Gly Leu Val Ala Ala Thr Ile
 39 1 5 10 15
 41 acg cca atg act gag aat gga gaa atc aac ttt tca gta att ggt cag 96
 42 Thr Pro Met Thr Glu Asn Gly Glu Ile Asn Phe Ser Val Ile Gly Gln
 43 20 25 30
 45 tat gtg gat tat ctt gtg aaa gaa cag gga gtg aag aac att ttt gtg 144
 46 Tyr Val Asp Tyr Leu Val Lys Glu Gln Gly Val Lys Asn Ile Phe Val
 47 35 40 45
 49 aat ggc aca aca gga gaa ggc ctg tcc ctg agc gtc tca gag cgt cgc 192
 50 Asn Gly Thr Thr Gly Glu Gly Leu Ser Leu Ser Val Ser Glu Arg Arg
 51 50 55 60
 53 cag gtt gca gag gag tgg gtg aca aaa ggg aag gac aag ctg gat cag 240
 54 Gln Val Ala Glu Glu Trp Val Thr Lys Gly Lys Asp Lys Leu Asp Gln
 55 65 70 75 80
 57 gtg ata att cac gta gga gca ctg agc ttg aag gag tca cag gaa ctg 288
 58 Val Ile Ile His Val Gly Ala Leu Ser Leu Lys Glu Ser Gln Glu Leu
 59 85 90 95
 61 gcc caa cat gca gca gaa ata gga gct gat ggc atc gct gtc att gca 336
 62 Ala Gln His Ala Ala Glu Ile Gly Ala Asp Gly Ile Ala Val Ile Ala
 63 100 105 110
 65 ccg ttc ttc ctc aag cca tgg acc aaa gat atc ctg att aat ttc cta 384
 66 Pro Phe Phe Leu Lys Pro Trp Thr Lys Asp Ile Leu Ile Asn Phe Leu
 67 115 120 125

Does Not Comply
 Corrected Diskette Needed

See page 3 of 7 and
 page 4 of 7

These types of errors may exist
 throughout the sequence listing.
 Please check subsequent sequences
 for similar errors.

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/930,440

DATE: 08/23/2001
 TIME: 16:49:26

Input Set : A:\PF509p2--SeqList.txt
 Output Set: N:\CRF3\08162001\I930440.raw

```

69 aag gaa gtg gct gct gcc gcc cct gcc ctg cca ttt tat tac tat cac 432
70 Lys Glu Val Ala Ala Ala Pro Ala Leu Pro Phe Tyr Tyr Tyr His
71 130 135 140
73 att cct gcc ttg aca ggg gta aag att cgt gct gag gag ttg ttg gat 480
74 Ile Pro Ala Leu Thr Gly Val Lys Ile Arg Ala Glu Glu Leu Leu Asp
75 145 150 155 160
77 ggg att ctg gat aag atc ccc acc ttc caa ggg ctg aaa ttc agt gat 528
78 Gly Ile Leu Asp Lys Ile Pro Thr Phe Gln Gly Leu Lys Phe Ser Asp
79 165 170 175
81 aca gat ctc tta gac ttc ggg caa tgt gtt gat cag aat cgc cag caa 576
82 Thr Asp Leu Leu Asp Phe Gly Gln Cys Val Asp Gln Asn Arg Gln Gln
83 180 185 190
85 cag ttt gct ttc ctt ttt ggg gtg gat gag caa ctg ttg agt gct ctg 624
86 Gln Phe Ala Phe Leu Phe Gly Val Asp Glu Gln Leu Leu Ser Ala Leu
87 195 200 205
89 gtg atg gga gca act gga gca gtg ggc agt ttt gta tcc aga gat tta 672
90 Val Met Gly Ala Thr Gly Ala Val Gly Ser Phe Val Ser Arg Asp Leu
91 210 215 220
93 tca act ttg ttg tca aac tag gttttggagt gtcacagacc aaagccatca 723
94 Ser Thr Leu Leu Ser Asn
95 225 230
97 tgactctggt ctctgggatt ccaatgggcc caccocggct tccactgcag aaagcctcca 783
99 gggagttttac tgatagtgcg gaagctaaac tgaagagcct ggatttcctt tctttcactg 843
101 atttaaagga tggaaacttg gaagctggta gctagtgcct ctctatcaaa tcagggtttg 903
103 cacttgaga cataatctac cttaaatagt gcattttttt ctcagggaat tttagatgaa 963
105 cttgaataaa ctctcctagc aaatgaaatc tcacaataag cattgaggta ccttttgatg 1023
107 gccttaaaaa gtcttatttt gtgaaggggc aaaaactota ggagtcacaa ctctcagtca 1083
109 ttcatttcac agattttttt gtggagaaat ttctgtttat atggatgaaa tggaaatcaag 1143
111 aggaaaattg taattgatta attccatctg tctttaggag ctctcattat ctcggtctct 1203
113 gggttcctaatt cctattttta agttgtctaa ttttaaacca ctataatatg tcttcatttt 1263
115 aataaatatt catttggaat ctaggaaaac tctgagctac tgcatttagg caggcacttt 1323
117 aataccaaac tgtaacatgt ctcaactgta tacaactcaa aatacaccag ctcaattggc 1383
119 tgetcagtct aactctagaa tggatgcttt tgaattcatt tcgatg 1429
122 <210> SEQ ID NO: 2
123 <211> LENGTH: 230
124 <212> TYPE: PRT
125 <213> ORGANISM: Homo sapiens
127 <400> SEQUENCE: 2
128 Met Ala Phe Pro Lys Lys Lys Leu Gln Gly Leu Val Ala Ala Thr Ile
129 1 5 10 15
130 Thr Pro Met Thr Glu Asn Gly Glu Ile Asn Phe Ser Val Ile Gly Gln
131 20 25 30
132 Tyr Val Asp Tyr Leu Val Lys Glu Gln Gly Val Lys Asn Ile Phe Val
133 35 40 45
134 Asn Gly Thr Thr Gly Glu Gly Leu Ser Leu Ser Val Ser Glu Arg Arg
135 50 55 60
136 Gln Val Ala Glu Glu Trp Val Thr Lys Gly Lys Asp Lys Leu Asp Gln
137 65 70 75 80
138 Val Ile Ile His Val Gly Ala Leu Ser Leu Lys Glu Ser Gln Glu Leu

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/930,440

DATE: 08/23/2001

TIME: 16:49:26

Input Set : A:\PF509p2--SeqList.txt

Output Set: N:\CRF3\08162001\I930440.raw

```

139          85          90          95
140 Ala Gln His Ala Ala Glu Ile Gly Ala Asp Gly Ile Ala Val Ile Ala
141          100          105          110
142 Pro Phe Phe Leu Lys Pro Trp Thr Lys Asp Ile Leu Ile Asn Phe Leu
143          115          120          125
144 Lys Glu Val Ala Ala Ala Ala Pro Ala Leu Pro Phe Tyr Tyr Tyr His
145          130          135          140
146 Ile Pro Ala Leu Thr Gly Val Lys Ile Arg Ala Glu Glu Leu Leu Asp
147 145          150          155          160
148 Gly Ile Leu Asp Lys Ile Pro Thr Phe Gln Gly Leu Lys Phe Ser Asp
149          165          170          175
150 Thr Asp Leu Leu Asp Phe Gly Gln Cys Val Asp Gln Asn Arg Gln Gln
151          180          185          190
152 Gln Phe Ala Phe Leu Phe Gly Val Asp Glu Gln Leu Leu Ser Ala Leu
153          195          200          205
154 Val Met Gly Ala Thr Gly Ala Val Gly Ser Phe Val Ser Arg Asp Leu
155          210          215          220
156 Ser Thr Leu Leu Ser Asn
157 225          230
161 <210> SEQ ID NO: 3
162 <211> LENGTH: 1305
163 <212> TYPE: DNA
164 <213> ORGANISM: Homo sapiens
166 <220> FEATURE:
167 <221> NAME/KEY: CDS
168 <222> LOCATION: (1)..(1305)
170 <220> FEATURE:
171 <221> NAME/KEY: Site
172 <222> LOCATION: (397)..(399)
173 <223> OTHER INFORMATION: Xaa equals His or Tyr
175 <220> FEATURE:
176 <221> NAME/KEY: Site
177 <222> LOCATION: (407)..(409)
178 <223> OTHER INFORMATION: Xaa equals Gly or Val
180 <220> FEATURE:
181 <221> NAME/KEY: Site
182 <222> LOCATION: (439)..(441)
183 <223> OTHER INFORMATION: Xaa equals Pro or Ser
185 <220> FEATURE:
186 <221> NAME/KEY: Site
187 <222> LOCATION: (505)..(507)
188 <223> OTHER INFORMATION: Xaa equals Gly or Val
190 <400> SEQUENCE: 3
191 atg gac tcg gtg gag aag ggg gcc gcc acc tcc gtc tcc aac ccg cgg 48
192 Met Asp Ser Val Glu Lys Gly Ala Ala Thr Ser Val Ser Asn Pro Arg
193 1 5 10 15
195 ggg cga ccg tcc cgg ggc cgg ccg ccg aag ctg cag cgc aac tct cgc 96
196 Gly Arg Pro Ser Arg Gly Arg Pro Pro Lys Leu Gln Arg Asn Ser Arg
197 20 25 30

```

Errored does not match sequence

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/930,440

DATE: 08/23/2001

TIME: 16:49:26

Input Set : A:\PF509p2--SeqList.txt

Output Set: N:\CRF3\08162001\I930440.raw

199	ggc	ggc	cag	ggc	cga	ggt	gtg	gag	aag	ccc	ccg	cac	ctg	gca	gcc	cta	144
200	Gly	Gly	Gln	Gly	Arg	Gly	Val	Glu	Lys	Pro	Pro	His	Leu	Ala	Ala	Leu	
201			35					40					45				
203	att	ctg	gcc	cgg	gga	ggc	agc	aaa	ggc	atc	ccc	ctg	aag	aac	att	aag	192
204	Ile	Leu	Ala	Arg	Gly	Gly	Ser	Lys	Gly	Ile	Pro	Leu	Lys	Asn	Ile	Lys	
205			50					55					60				
207	cac	ctg	gcg	ggg	gtc	ccg	ctc	att	ggc	tgg	gtc	ctg	cgt	gcg	gcc	ctg	240
208	His	Leu	Ala	Gly	Val	Pro	Leu	Ile	Gly	Trp	Val	Leu	Arg	Ala	Ala	Leu	
209	65					70					75				80		
211	gat	tca	ggg	gcc	ttc	cag	agt	gta	tgg	gtt	tcg	aca	gac	cat	gat	gaa	288
212	Asp	Ser	Gly	Ala	Phe	Gln	Ser	Val	Trp	Val	Ser	Thr	Asp	His	Asp	Glu	
213					85						90				95		
215	att	gag	aat	gtg	gcc	aaa	caa	ttt	ggt	gca	caa	gtt	cat	cga	aga	agt	336
216	Ile	Glu	Asn	Val	Ala	Lys	Gln	Phe	Gly	Ala	Gln	Val	His	Arg	Arg	Ser	
217				100					105				110				
219	tct	gaa	gtt	tca	aaa	gac	agc	tct	acc	tca	cta	gat	gcc	atc	ata	gaa	384
220	Ser	Glu	Val	Ser	Lys	Asp	Ser	Ser	Thr	Ser	Leu	Asp	Ala	Ile	Ile	Glu	
221			115					120				125					
223	ttt	ctt	aat	tat	OK	aat	gag	gkt	gac	att	gta	gga	aat	att	caa	gct	432
W--> 224	Phe	Leu	Asn	Tyr	Xaa	Asn	Glu	Xaa	Asp	Ile	Val	Gly	Asn	Ile	Gln	Ala	
225			130					135				140					
227	act	tct	yca	tgt	OK	tta	cat	cct	act	gat	ctt	caa	aaa	gtt	gca	gaa	480
W--> 228	Thr	Ser	Xaa	Cys	Leu	His	Pro	Thr	Asp	Leu	Gln	Lys	Val	Ala	Glu	Met	
229	145					150			OK		155					160	
231	att	cga	gaa	gaa	gga	tat	gat	tct	gkt	ttc	tct	gtt	gtg	aga	cgc	cat	528
W--> 232	Ile	Arg	Glu	Glu	Gly	Tyr	Asp	Ser	Xaa	Phe	Ser	Val	Val	Arg	Arg	His	
233					165				170						175		
235	cag	ttt	cga	tgg	agt	gaa	att	cag	aaa	gga	gtt	cgt	gaa	gtg	acc	gaa	576
236	Gln	Phe	Arg	Trp	Ser	Glu	Ile	Gln	Lys	Gly	Val	Arg	Glu	Val	Thr	Glu	
237				180					185					190			
239	cct	ctg	aat	tta	aat	cca	gct	aaa	cgg	cct	cgt	cga	caa	gac	tgg	gat	624
240	Pro	Leu	Asn	Leu	Asn	Pro	Ala	Lys	Arg	Pro	Arg	Arg	Gln	Asp	Trp	Asp	
241				195				200					205				
243	gga	gaa	tta	tat	gaa	aat	ggc	tca	ttt	tat	ttt	gct	aaa	aga	cat	ttg	672
244	Gly	Glu	Leu	Tyr	Glu	Asn	Gly	Ser	Phe	Tyr	Phe	Ala	Lys	Arg	His	Leu	
245			210				215					220					
247	ata	gag	atg	ggt	tac	ttg	cag	ggt	gga	aaa	tgg	cat	act	acg	aaa	tgc	720
248	Ile	Glu	Met	Gly	Tyr	Leu	Gln	Gly	Gly	Lys	Trp	His	Thr	Thr	Lys	Cys	
249	225					230					235					240	
251	gag	ctg	gaa	cat	agt	gtg	gat	ata	gat	gtg	gat	att	gat	tgg	cct	att	768
252	Glu	Leu	Glu	His	Ser	Val	Asp	Ile	Asp	Val	Asp	Ile	Asp	Trp	Pro	Ile	
253					245					250					255		
255	gca	gag	caa	aga	gta	tta	aga	tat	ggc	tat	ttt	ggc	aaa	gag	aag	ctt	816
256	Ala	Glu	Gln	Arg	Val	Leu	Arg	Tyr	Gly	Tyr	Phe	Gly	Lys	Glu	Lys	Leu	
257				260					265					270			
259	aag	gaa	ata	aaa	ctt	ttg	gtt	tgc	aat	att	gat	gga	tgt	ctc	acc	aat	864
260	Lys	Glu	Ile	Lys	Leu	Leu	Val	Cys	Asn	Ile	Asp	Gly	Cys	Leu	Thr	Asn	
261			275					280					285				
263	ggc	cac	att	tat	gta	tca	gga	gac	caa	aaa	gaa	ata	ata	tct	tat	gat	912

position
(406... 408)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/930,440

DATE: 08/23/2001

TIME: 16:49:26

Input Set : A:\PF509p2--SeqList.txt

Output Set: N:\CRF3\08162001\I930440.raw

```

264 Gly His Ile Tyr Val Ser Gly Asp Gln Lys Glu Ile Ile Ser Tyr Asp
265      290      295      300
267 gta aaa gat gct att ggg ata agt tta tta aag aaa agt ggt att gag 960
268 Val Lys Asp Ala Ile Gly Ile Ser Leu Leu Lys Lys Ser Gly Ile Glu
269 305      310      315      320
271 gtg agg cta atc tca gaa agg gcc tgt tca aag cag acg ctg tct tct 1008
272 Val Arg Leu Ile Ser Glu Arg Ala Cys Ser Lys Gln Thr Leu Ser Ser
273      325      330      335
275 tta aaa ctg gat tgc aaa atg gaa gtc agt gta tca gac aag cta gca 1056
276 Leu Lys Leu Asp Cys Lys Met Glu Val Ser Val Ser Asp Lys Leu Ala
277      340      345      350
279 gtt gta gat gaa tgg aga aaa gaa atg ggc ctg tgc tgg aaa gaa gtg 1104
280 Val Val Asp Glu Trp Arg Lys Glu Met Gly Leu Cys Trp Lys Glu Val
281      355      360      365
283 gca tat ctt gga aat gaa gtg tct gat gaa gag tgc ttg aag aga gtg 1152
284 Ala Tyr Leu Gly Asn Glu Val Ser Asp Glu Glu Cys Leu Lys Arg Val
285      370      375      380
287 ggc cta agt ggc gct cct gct gat gcc tgt tcc tac gcc cag aag gct 1200
288 Gly Leu Ser Gly Ala Pro Ala Asp Ala Cys Ser Tyr Ala Gln Lys Ala
289 385      390      395      400
291 gtt gga tac att tgc aaa tgt aat ggt ggc cgt ggt gcc atc cga gaa 1248
292 Val Gly Tyr Ile Cys Lys Cys Asn Gly Gly Arg Gly Ala Ile Arg Glu
293      405      410      415
295 ttt gca gag cac att tgc cta cta atg gaa aaa gtt aat aat tca tgc 1296
296 Phe Ala Glu His Ile Cys Leu Leu Met Glu Lys Val Asn Asn Ser Cys
297      420      425      430
299 caa aaa tag 1305
300 Gln Lys
303 <210> SEQ ID NO: 4
304 <211> LENGTH: 434
305 <212> TYPE: PRT
306 <213> ORGANISM: Homo sapiens
308 <220> FEATURE:
309 <221> NAME/KEY: Site
310 <222> LOCATION: (133)
311 <223> OTHER INFORMATION: Xaa equals His or Tyr
313 <220> FEATURE:
314 <221> NAME/KEY: Site
315 <222> LOCATION: (136)
316 <223> OTHER INFORMATION: Xaa equals Gly or Val
318 <220> FEATURE:
319 <221> NAME/KEY: Site
320 <222> LOCATION: (147)
321 <223> OTHER INFORMATION: Xaa equals Pro or Ser
323 <220> FEATURE:
324 <221> NAME/KEY: Site
325 <222> LOCATION: (169)
326 <223> OTHER INFORMATION: Xaa equals Gly or Val
328 <400> SEQUENCE: 4

```

VERIFICATION SUMMARY

DATE: 08/23/2001

PATENT APPLICATION: US/09/930,440

TIME: 16:49:27

Input Set : A:\PF509p2--SeqList.txt

Output Set: N:\CRF3\08162001\I930440.raw

L:8 M:270 C: Current Application Number differs, Replaced Current Application Number

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

L:349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4